

0070777-000026SEQLIST.txt  
SEQUENCE LISTING

<110> Genomine, Inc.  
POSTECH FOUNDATION

<120> Novel Phytochrome-interacting protein and a use thereof

<130> OP05-1002

<150> KR10-2004-0013663  
<151> 2004-02-27

<160> 26

<170> KopatentIn 1.71

<210> 1  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer

<400> 1  
ggatccaaat gtcaggctct aggccgact 29

<210> 2  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer

<400> 2  
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<210> 3  
<211> 1455  
<212> DNA  
<213> Arabidopsis thaliana

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atggagacca agaatgagaa ttctgatgtt tcacgggcag aggagttaa aagtcaggcc 60  
aacgaagctt ttaaaggcca caaatactcc agtgctattg atctatatac aaaagctatt 120  
gaactcaaca gcaacaacgc tgtgtattgg gcaaatacgtg catttgctca cacaaaactg 180  
gaggaatatg gcagtgcaat acaggatgca tcgaaggcca ttgaagttga ttcaagatac 240  
tctaagggtt attacaggcg tgggtgctgcg tatcttgcca tgggaaaatt taaggatgcc 300  
ttgaaggact tccaacaggt aaaaaggctt tctcctaata accctgatgc cacaagaaag 360  
ctaaaggaat gtgagaaagc agtgatgaaa ctcaaatttg aagaagcaat ctctgtgcc 420  
gtatctgaaa ggcgttcagt agctgagtc attgacttcc atacaataga ggttgagcca 480  
caatattctg gtgctagaat tgaggagag gaagttacct tagattttgt gaaaacgatg 540  
atggaggatt ttaagaacca aaaaacattg cataaacggt atgcctatca aatcgtctta 600

## 0070777-000026SEQLIST.txt

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cagactaggc aaatcttgct agcactgcct tctcttggtg atataagtgt tccacatggc      660
aaacatatca ctgtttgcgg tgacgttcat ggtcagttct acgatcttct caatatcttt      720
gagcttaatg gcctcccttc ggaggagaac ccatacctat ttaatggcga ctttgtggac      780
agaggctcat tctccgttga gatcatcctc actttgtttg ctttcaagtg catgtgccca      840
tcatccatat atctagccag aggaaacat gaaagcaaga gcatgaacaa aatttatggt      900
tttgaggggtg aggttcgggtc caagttgagt gaaaaattcg tggatctctt tgctgaagtt      960
ttctgttacc tcccgttggc tcatgttata aatgggaagg tcttcgtggt acatggaggt    1020
cttttcagtg ttgacggcgt gaaactctca gacatcagag ccattgacag attctgtgag    1080
ccaccagagg aaggactaat gtgtgaacta ttgtggagt atcctcaacc tctccctgga    1140
agaggcccaa gcaagcgagg agttggtcta tcatttggtg gagatgtgac aaagaggttt    1200
ttgcaagata acaattttaga ttgtttggtc cggtcacatg aagtaaaaga tgaaggttat    1260
gaggttgaac atgacggtaa actcataact gtcttctctg cgccaaatta ctgtgatcag    1320
atgggtaata agggagcctt cattcgtttt gaagctcctg atatgaagcc aaacattggt    1380
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aggatgttca actaa                                           1455

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<210>      4
<211>     484
<212>      PRT
<213>      Arabidopsis thaliana

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Lys Ser Gln Ala Asn Glu Ala Phe Lys Gly His Lys Tyr Ser Ser Ala
          20          25          30
Ile Asp Leu Tyr Thr Lys Ala Ile Glu Leu Asn Ser Asn Asn Ala Val
          35          40          45
Tyr Trp Ala Asn Arg Ala Phe Ala His Thr Lys Leu Glu Glu Tyr Gly
          50          55          60
Ser Ala Ile Gln Asp Ala Ser Lys Ala Ile Glu Val Asp Ser Arg Tyr
          65          70          75          80
Ser Lys Gly Tyr Tyr Arg Arg Gly Ala Ala Tyr Leu Ala Met Gly Lys
          85          90          95
Phe Lys Asp Ala Leu Lys Asp Phe Gln Gln Val Lys Arg Leu Ser Pro
          100          105          110
Asn Asp Pro Asp Ala Thr Arg Lys Leu Lys Glu Cys Glu Lys Ala Val
          115          120          125
Met Lys Leu Lys Phe Glu Glu Ala Ile Ser Val Pro Val Ser Glu Arg
          130          135          140
Arg Ser Val Ala Glu Ser Ile Asp Phe His Thr Ile Glu Val Glu Pro
          145          150          155          160

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Gln Tyr Ser Gly Ala Arg Ile Glu Gly Glu Glu Val Thr Leu Asp Phe  
 165 170 175  
 Val Lys Thr Met Met Glu Asp Phe Lys Asn Gln Lys Thr Leu His Lys  
 180 185 190  
 Arg Tyr Ala Tyr Gln Ile Val Leu Gln Thr Arg Gln Ile Leu Leu Ala  
 195 200 205  
 Leu Pro Ser Leu Val Asp Ile Ser Val Pro His Gly Lys His Ile Thr  
 210 215 220  
 Val Cys Gly Asp Val His Gly Gln Phe Tyr Asp Leu Leu Asn Ile Phe  
 225 230 235 240  
 Glu Leu Asn Gly Leu Pro Ser Glu Glu Asn Pro Tyr Leu Phe Asn Gly  
 245 250 255  
 Asp Phe Val Asp Arg Gly Ser Phe Ser Val Glu Ile Ile Leu Thr Leu  
 260 265 270  
 Phe Ala Phe Lys Cys Met Cys Pro Ser Ser Ile Tyr Leu Ala Arg Gly  
 275 280 285  
 Asn His Glu Ser Lys Ser Met Asn Lys Ile Tyr Gly Phe Glu Gly Glu  
 290 295 300  
 Val Arg Ser Lys Leu Ser Glu Lys Phe Val Asp Leu Phe Ala Glu Val  
 305 310 315 320  
 Phe Cys Tyr Leu Pro Leu Ala His Val Ile Asn Gly Lys Val Phe Val  
 325 330 335  
 Val His Gly Gly Leu Phe Ser Val Asp Gly Val Lys Leu Ser Asp Ile  
 340 345 350  
 Arg Ala Ile Asp Arg Phe Cys Glu Pro Pro Glu Glu Gly Leu Met Cys  
 355 360 365  
 Glu Leu Leu Trp Ser Asp Pro Gln Pro Leu Pro Gly Arg Gly Pro Ser  
 370 375 380  
 Lys Arg Gly Val Gly Leu Ser Phe Gly Gly Asp Val Thr Lys Arg Phe  
 385 390 395 400  
 Leu Gln Asp Asn Asn Leu Asp Leu Leu Val Arg Ser His Glu Val Lys  
 405 410 415  
 Asp Glu Gly Tyr Glu Val Glu His Asp Gly Lys Leu Ile Thr Val Phe  
 420 425 430  
 Ser Ala Pro Asn Tyr Cys Asp Gln Met Gly Asn Lys Gly Ala Phe Ile  
 435 440 445  
 Arg Phe Glu Ala Pro Asp Met Lys Pro Asn Ile Val Thr Phe Ser Ala  
 450 455 460  
 Val Pro His Pro Asp Val Lys Pro Met Ala Tyr Ala Asn Asn Phe Leu  
 465 470 475 480  
 Arg Met Phe Asn

<210> 5  
 <211> 24  
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 <213> Artificial Sequence

<220>  
 <223> PCR primer

<400> 5  
 ggatccatgg agaccaagaa tgag 24

<210> 6  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> PCR primer

<400> 6  
 ctcgagttag ttgaacatcc tgag 24

<210> 7  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> PCR primer

<400> 7  
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<210> 8  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> PCR primer

<400> 8  
 gctgatcagc atggtttccg gagtcggggg tagt 34

<210> 9  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> PCR primer

<400> 9  
 cccggccgga ctaatatggc atcatcagca tcat 34

<210> 10  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> PCR primer

<400> 10  
ctcgagtcaa gagattgctt cttcaaa 27

<210> 11  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer

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ggatccatgc cagtatctga aaggcgt 27

<210> 12  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer

<400> 12  
atggagacca agaatgagaa ttct 24

<210> 13  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer

<400> 13  
ttagttgaac atcctgagaa agtt 24

<210> 14  
<211> 347  
<212> PRT  
<213> Arabidopsis thaliana

<400> 14  
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1 5 10 15  
His Thr Ile Glu Val Glu Pro Gln Tyr Ser Gly Ala Arg Ile Glu Gly  
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Glu Glu Val Thr Leu Asp Phe Val Lys Thr Met Met Glu Asp Phe Lys  
35 40 45  
Asn Gln Lys Thr Leu His Lys Arg Tyr Ala Tyr Gln Ile Val Leu Gln  
50 55 60  
Thr Arg Gln Ile Leu Leu Ala Leu Pro Ser Leu Val Asp Ile Ser Val  
65 70 75 80  
Pro His Gly Lys His Ile Thr Val Cys Gly Asp Val His Gly Gln Phe  
85 90 95

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Tyr Asp Leu Leu Asn Ile Phe Glu Leu Asn Gly Leu Pro Ser Glu Glu  
100 105 110  
Asn Pro Tyr Leu Phe Asn Gly Asp Phe Val Asp Arg Gly Ser Phe Ser  
115 120 125  
Val Glu Ile Ile Leu Thr Leu Phe Ala Phe Lys Cys Met Cys Pro Ser  
130 135 140  
Ser Ile Tyr Leu Ala Arg Gly Asn His Glu Ser Lys Ser Met Asn Lys  
145 150 155 160  
Ile Tyr Gly Phe Glu Gly Glu Val Arg Ser Lys Leu Ser Glu Lys Phe  
165 170 175  
Val Asp Leu Phe Ala Glu Val Phe Cys Tyr Leu Pro Leu Ala His Val  
180 185 190  
Ile Asn Gly Lys Val Phe Val Val His Gly Gly Leu Phe Ser Val Asp  
195 200 205  
Gly Val Lys Leu Ser Asp Ile Arg Ala Ile Asp Arg Phe Cys Glu Pro  
210 215 220  
Pro Glu Glu Gly Leu Met Cys Glu Leu Leu Trp Ser Asp Pro Gln Pro  
225 230 235 240  
Leu Pro Gly Arg Gly Pro Ser Lys Arg Gly Val Gly Leu Ser Phe Gly  
245 250 255  
Gly Asp Val Thr Lys Arg Phe Leu Gln Asp Asn Asn Leu Asp Leu Leu  
260 265 270  
Val Arg Ser His Glu Val Lys Asp Glu Gly Tyr Glu Val Glu His Asp  
275 280 285  
Gly Lys Leu Ile Thr Val Phe Ser Ala Pro Asn Tyr Cys Asp Gln Met  
290 295 300  
Gly Asn Lys Gly Ala Phe Ile Arg Phe Glu Ala Pro Asp Met Lys Pro  
305 310 315 320  
Asn Ile Val Thr Phe Ser Ala Val Pro His Pro Asp Val Lys Pro Met  
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Ala Tyr Ala Asn Asn Phe Leu Arg Met Phe Asn  
340 345

<210> 15  
<211> 1041  
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<213> Arabidopsis thaliana

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acgatgatgg aggattttta gaaccaaaaa acattgcata aacggtatgc ctatcaaadc 180  
gtcttacaga ctaggcaaat cttgctagca ctgcccttctc ttgttgatat aagtgttcca 240  
catggcaaac atatcactgt ttgcggtgac gttcatgggtc agttctacga tcttctcaat 300  
atctttgagc ttaatggcct cccttcggag gagaacccat acctatttaa tggcgacttt 360

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gtggacagag gctcattctc cgttgagatc atcctcactt tgtttgcttt caagtgcattg      420
tgcccatcat ccatatatct agccagagga aaccatgaaa gcaagagcat gaacaaaatt      480
tatggttttg aggggtgaggt tcgggtccaag ttgagtgaaa aattcgtgga tctctttgct      540
gaagttttct gttacctccc gttggctcat gttataaatg ggaaggtctt cgtgggtacat      600
ggaggtcttt tcagtgttga cggcgtgaaa ctctcagaca tcagagccat tgacagattc      660
tgtgagccac cagaggaagg actaatgtgt gaactattgt ggagtgatcc tcaacctctc      720
cctggaagag gccaagcaa gcgaggagtt ggtctatcat ttgggtggaga tgtgacaaag      780
aggtttttgc aagataacaa tttagatttg ttgggtccggt cacatgaagt aaaagatgaa      840
ggttatgagg ttgaacatga cggtaaactc ataactgtct tctctgcgcc aaattactgt      900
gatcagatgg gtaataaggg agccttcatt cgttttgaag ctctgatat gaagccaaac      960
attgttacat tctcagcagt gcctcatccg gatgtgaagc ctatggcata tgcaaacaac     1020
tttctcagga tgttcaacta a                                           1041

```

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<210>      16
<211>      479
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<213>      Homo sapiens

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<220>
<221>      PEPTIDE
<222>      (1)
<223>      PAPP5

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  1          5          10          15
Lys Ser Gln Ala Asn Glu Ala Phe Lys Gly His Lys Tyr Ser Ser Ala
          20          25          30
Ile Asp Leu Tyr Thr Lys Ala Ile Glu Leu Asn Ser Asn Asn Ala Val
          35          40          45
Tyr Trp Ala Asn Arg Ala Phe Ala His Thr Lys Leu Glu Glu Tyr Gly
          50          55          60
Ser Ala Ile Gln Asp Ala Ser Lys Ala Ile Glu Val Asp Ser Arg Tyr
          65          70          75          80
Ser Lys Gly Tyr Tyr Arg Arg Gly Ala Ala Tyr Leu Ala Met Gly Lys
          85          90          95
Glu Lys Asp Ala Leu Lys Asp Phe Gln Gln Val Lys Gly Leu Ser Pro
          100          105          110
Asn Asp Pro Asp Ala Thr Arg Lys Leu Lys Glu Cys Glu Lys Ala Val
          115          120          125
Met Lys Leu Lys Phe Glu Glu Ala Ile Ser Val Pro Val Ser Glu Arg
          130          135          140
Arg Ser Val Ala Glu Ser Ile Asp Phe His Thr Ile Glu Val Glu Pro
          145          150          155          160
Gln Tyr Ser Gly Ala Arg Ile Glu Gly Glu Glu Val Thr Leu Asp Phe

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165

170

175

Val Lys Thr Met Met Glu Asp Phe Lys Asn Gln Lys Thr Leu His Lys  
 180 185 190  
 Arg Tyr Ala Tyr Gln Ile Val Leu Gln Thr Arg Gln Ile Leu Leu Ala  
 195 200 205  
 Leu Pro Ser Leu Val Asp Ile Ser Val Pro His Gly Lys His Ile Thr  
 210 215 220  
 Val Cys Gly Asp Val His Gly Gln Phe Tyr Asp Leu Leu Asn Ile Phe  
 225 230 235 240  
 Glu Asp Asn Gly Leu Pro Ser Glu Glu Asn Pro Tyr Leu Phe Asn Gly  
 245 250 255  
 Asp Phe Val Asp Arg Gly Ser Phe Ser Val Glu Ile Ile Leu Thr Leu  
 260 265 270  
 Phe Ala Glu Lys Cys Met Cys Pro Ser Ser Ile Tyr Leu Ala Arg Gly  
 275 280 285  
 Asn His Glu Ser Lys Ser Met Asn Lys Ile Tyr Gly Phe Glu Gly Glu  
 290 295 300  
 Val Arg Ser Lys Leu Ser Glu Lys Phe Val Asp Leu Phe Ala Glu Val  
 305 310 315 320  
 Phe Cys Tyr Leu Pro Leu Ala His Val Ile Asn Gly Lys Val Phe Val  
 325 330 335  
 Val His Gly Gly Leu Phe Ser Val Asp Gly Val Lys Leu Ser Asp Ile  
 340 345 350  
 Arg Ala Ile Asp Arg Phe Cys Glu Pro Phe Glu Glu Gly Leu Met Cys  
 355 360 365  
 Glu Leu Leu Trp Ser Asp Pro Gln Pro Leu Pro Gly Arg Gly Pro Ser  
 370 375 380  
 Lys Arg Gly Val Gly Leu Ser Phe Gly Gly Asp Val Thr Lys Arg Phe  
 385 390 395 400  
 Leu Gln Asp Asn Asn Leu Asp Leu Leu Val Arg Ser His Glu Val Lys  
 405 410 415  
 Asp Glu Gly Tyr Glu Val Glu His Asp Gly Lys Leu Ile Thr Val Phe  
 420 425 430  
 Ser Ala Pro Asn Cys Asp Gln Met Gly Asn Lys Gly Ala Phe Ile Arg  
 435 440 445  
 Phe Glu Ala Pro Asp Met Lys Pro Asn Ile Val Thr Phe Ser Ala Val  
 450 455 460  
 Pro His Pro Met Ala Tyr Ala Asn Asn Phe Ile Arg Met Phe Asn  
 465 470 475

<210> 17  
 <211> 492  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> PEPTIDE  
 <222> (1)



&lt;223&gt; PP5

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 Phe Lys Ala Lys Asp Tyr Glu Asn Ala Ile Lys Phe Tyr Ser Gln Ala  
 35 40 45  
 Ile Glu Leu Asn Pro Ser Asn Ala Ile Tyr Tyr Gly Asn Arg Ser Leu  
 50 55 60  
 Ala Tyr Leu Arg Thr Glu Cys Tyr Gly Tyr Ala Leu Gly Asp Ala Thr  
 65 70 75 80  
 Arg Ala Ile Glu Leu Asp Lys Lys Tyr Ile Lys Gly Tyr Tyr Arg Arg  
 85 90 95  
 Ala Ala Ser Asn Met Ala Leu Gly Lys Phe Arg Ala Ala Leu Arg Asp  
 100 105 110  
 Tyr Glu Thr Val Val Lys Val Lys Pro His Asp Lys Asp Ala Lys Met  
 115 120 125  
 Lys Tyr Gln Glu Cys Asn Lys Thr Val Lys Gln Lys Ala Phe Glu Arg  
 130 135 140  
 Ala Ile Gly Asp Glu His Lys Arg Ser Val Val Asp Ser Leu Asp Ile  
 145 150 155 160  
 Glu Ser Met Thr Ile Glu Asp Glu Tyr Ser Gly Pro Lys Leu Glu Asp  
 165 170 175  
 Gly Lys Val Thr Ile Ser Phe Met Lys Glu Leu Met Gln Trp Tyr Lys  
 180 185 190  
 Asp Gln Lys Lys Leu His Arg Lys Cys Ala Tyr Gln Ile Leu Val Gln  
 195 200 205  
 Val Lys Glu Val Leu Ser Lys Leu Ser Thr Leu Val Glu Thr Thr Leu  
 210 215 220  
 Lys Glu Thr Glu Lys Ile Thr Val Cys Gly Asp Thr His Gly Gln Phe  
 225 230 235 240  
 Tyr Asp Leu Leu Asn Ile Phe Glu Leu Asn Gly Leu Pro Ser Glu Thr  
 245 250 255  
 Asn Pro Tyr Asp Phe Asn Gly Asp Phe Val Asp Arg Gly Ser Phe Ser  
 260 265 270  
 Val Glu Val Ile Leu Thr Leu Phe Gly Phe Lys Leu Leu Tyr Pro Asp  
 275 280 285  
 His Phe His Leu Leu Arg Gly Asn His Glu Thr Asp Asn Met Asn Gln  
 290 295 300  
 Ile Tyr Gly Phe Glu Gly Glu Val Lys Ala Lys Tyr Thr Ala Gln Met  
 305 310 315 320  
 Tyr Glu Leu Phe Ser Glu Val Phe Glu Trp Leu Pro Leu Ala Gln Cys  
 325 330 335  
 Ile Asn Gly Lys Val Leu Ile Met His Gly Gly Leu Phe Ser Glu Asp

340

345

350

Gly Val Thr Leu Asp Asp Ile Arg Lys Ile Glu Arg Asn Arg Gln Pro  
           355                          360                          365  
 Phe Asp Ser Gly Pro Met Cys Asp Leu Leu Trp Ser Asp Pro Gln Pro  
           370                          375                          380  
 Gln Asn Gly Arg Ser Ile Ser Lys Arg Gly Val Ser Cys Gln Phe Gly  
   385                          390                          395                          400  
 Pro Asp Val Thr Lys Ala Phe Leu Glu Glu Asn Asn Leu Asp Tyr Ile  
                           405                          410                          415  
 Ile Arg Ser His Glu Val Lys Ala Glu Gly Tyr Glu Val Ala His Gly  
                           420                          425                          430  
 Gly Arg Cys Val Thr Val Phe Ser Ala Pro Asn Tyr Cys Asp Gln Met  
           435                          440                          445  
 Gly Asn Lys Ala Ser Tyr Ile His Leu Gln Gly Ser Asp Leu Arg Pro  
   450                          455                          460  
 Gln Phe His Gln Phe Thr Ala Val Pro His Pro Asn Val Lys Pro Met  
   465                          470                          475                          480  
 Ala Tyr Ala Asn Thr Leu Leu Gln Leu Gly Met Met  
                           485                          490

<210> 18  
 <211> 500  
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 <213> Mus musculus  
  
 <220>  
 <221> PEPTIDE  
 <222> (1)  
 <223> PP5

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                           20                          25                          30  
 Thr Gln Ala Asn Asp Tyr Phe Lys Ala Lys Asp Tyr Glu Asn Ala Ile  
           35                          40                          45  
 Lys Phe Tyr Ser Gln Ala Ile Glu Leu Asn Pro Gly Asn Ala Ile Tyr  
   50                          55                          60  
 Tyr Gly Asn Arg Ser Leu Ala Tyr Leu Arg Thr Glu Cys Tyr Gly Tyr  
   65                          70                          75                          80  
 Ala Leu Gly Asp Ala Thr Arg Ala Ile Glu Leu Asp Lys Lys Tyr Ile  
                           85                          90                          95  
 Lys Gly Tyr Tyr Arg Arg Ala Ala Ser Asn Met Ala Leu Gly Lys Phe  
           100                          105                          110  
 Arg Ala Ala Leu Arg Asp Tyr Glu Thr Val Val Lys Val Lys Pro Asn  
   115                          120                          125  
 Asp Lys Asp Ala Lys Met Lys Tyr Gln Glu Cys Ser Lys Thr Val Lys  
   130                          135                          140

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Gln Lys Ala Phe Glu Arg Ala Ile Ala Gly Asp Glu His Arg Arg Ser  
 145 150 155 160  
 Val Val Asp Ser Leu Asp Ile Glu Ser Met Thr Ile Glu Asp Glu Tyr  
 165 170 175  
 Ser Gly Pro Lys Leu Glu Asp Gly Lys Val Thr Ile Thr Phe Met Lys  
 180 185 190  
 Asp Leu Met Gln Trp Tyr Lys Asp Gln Lys Lys Leu His Arg Lys Cys  
 195 200 205  
 Ala Tyr Gln Ile Leu Val Gln Val Lys Glu Val Leu Cys Lys Leu Ser  
 210 215 220  
 Thr Leu Val Glu Thr Thr Leu Lys Glu Thr Glu Lys Ile Thr Val Cys  
 225 230 235 240  
 Gly Asp Thr His Gly Gln Phe Tyr Asp Leu Leu Asn Ile Phe Glu Leu  
 245 250 255  
 Asn Gly Leu Pro Ser Glu Thr Thr Asn Pro Tyr Thr Phe Asn Gly Asp  
 260 265 270  
 Phe Val Asp Arg Gly Ser Phe Ser Val Glu Val Ile Leu Thr Leu Phe  
 275 280 285  
 Gly Phe Lys Leu Leu Tyr Pro Asp His Phe His Leu Leu Arg Gly Asn  
 290 295 300  
 His Glu Thr Asp Asn Met Asn Gln Ile Tyr Gly Phe Glu Gly Glu Val  
 305 310 315 320  
 Lys Ala Lys Tyr Thr Ala Gln Met Tyr Glu Leu Phe Ser Glu Val Glu  
 325 330 335  
 Glu Trp Leu Pro Leu Ala Gln Cys Ile Asn Gly Lys Val Leu Ile Met  
 340 345 350  
 His Gly Gly Leu Phe Ser Glu Asp Gly Val Thr Leu Asp Asp Ile Arg  
 355 360 365  
 Lys Ile Glu Arg Asn Arg Gln Pro Pro Asp Ser Gly Pro Met Cys Asp  
 370 375 380  
 Leu Leu Trp Ser Asp Pro Gln Pro Gln Asn Gly Arg Ser Val Ser Lys  
 385 390 395 400  
 Arg Gly Val Ser Cys Gln Phe Gly Pro Asp Val Thr Lys Ala Phe Leu  
 405 410 415  
 Glu Glu Asn Gln Leu Asp Tyr Ile Ile Arg Ser His Glu Val Lys Ala  
 420 425 430  
 Glu Gly Tyr Glu Val Ala His Gly Gly Arg Cys Val Thr Val Phe Ser  
 435 440 445  
 Ala Pro Asn Tyr Cys Asp Gln Met Gly Asn Lys Ala Ser Tyr Ile His  
 450 455 460  
 Leu Gln Gly Ser Asp Leu Arg Pro Gln Phe His Gln Phe Thr Ala Val  
 465 470 475 480  
 Pro His Pro Asn Val Lys Pro Met Ala Tyr Ala Asn Thr Leu Leu Gln  
 485 490 495  
 Leu Gly Met Met

500

<210> 19  
 <211> 497  
 <212> PRT  
 <213> Rattus norvegicus

<220>  
 <221> PEPTIDE  
 <222> (1)  
 <223> PP5

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 Asp Asp Pro Pro Ala Glu Gly Thr Leu Lys Arg Ala Glu Glu Leu Lys  
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 35 40 45  
 Lys Phe Tyr Ser Gln Ala Ile Glu Leu Asn Pro Ser Asn Ala Ile Tyr  
 50 55 60  
 Tyr Gly Asn Arg Ser Leu Ala Tyr Leu Arg Thr Glu Cys Tyr Gly Tyr  
 65 70 75 80  
 Ala Leu Gly Asp Ala Thr Arg Ala Ile Glu Leu Asp Lys Lys Tyr Ile  
 85 90 95  
 Lys Gly Tyr Tyr Arg Arg Ala Ala Ser Asn Met Ala Leu Gly Lys Phe  
 100 105 110  
 Arg Ala Ala Leu Arg Asp Tyr Glu Thr Val Val Lys Pro Asn Asp Lys  
 115 120 125  
 Asp Ala Lys Met Lys Tyr Gln Glu Cys Ser Lys Thr Val Lys Gln Lys  
 130 135 140  
 Gln Phe Glu Arg Ala Ile Ala Gly Asp Glu His Arg Arg Ser Val Val  
 145 150 155 160  
 Asp Ser Leu Asp Ile Glu Ser Met Thr Leu Glu Asp Glu Tyr Ser Gly  
 165 170 175  
 Pro Lys Leu Glu Asp Gly Lys Val Thr Ile Thr Phe Met Lys Asp Leu  
 180 185 190  
 Met Gln Trp Tyr Lys Asp Gln Lys Lys Leu His Arg Lys Cys Ala Tyr  
 195 200 205  
 Gln Ile Leu Val Gln Val Lys Glu Val Leu Val Lys Leu Ser Thr Leu  
 210 215 220  
 Val Glu Thr Thr Leu Lys Glu Thr Glu Lys Ile Thr Val Cys Gly Asp  
 225 230 235 240  
 Thr His Gly Gln Phe Tyr Asp Leu Leu Asn Glu Phe Glu Leu Asn Gly  
 245 250 255  
 Leu Pro Ser Glu Thr Asn Pro Tyr Ile Glu Asn Gly Asp Phe Val Asp  
 260 265 270  
 Arg Gly Ser Phe Ser Val Glu Val Ile Leu Thr Leu Phe Gly Phe Lys  
 275 280 285

## 0070777-000026SEQLIST.txt

Leu Leu Tyr Pro Asp His Phe His Leu Leu Arg Gly Asn His Glu Thr  
 290 295 300  
 Asp Asn Met Asn Gln Ile Tyr Gly Phe Glu Gly Glu Val Lys Ala Lys  
 305 310 315 320  
 Tyr Thr Ala Gln Met Tyr Glu Leu Phe Ser Glu Val Glu Glu Trp Leu  
 325 330 335  
 Pro Leu Ala Gln Cys Ile Asn Gly Lys Val Leu Ile Met His Gly Gly  
 340 345 350  
 Leu Phe Ser Glu Asp Gly Val Thr Leu Asp Asp Ile Pro Lys Ile Glu  
 355 360 365  
 Arg Asn Arg Gln Pro Phe Asp Ser Gly Pro Met Cys Asp Leu Leu Trp  
 370 375 380  
 Ser Asp Pro Gln Pro Gln Asn Gly Arg Ser Val Ser Lys Arg Gly Val  
 385 390 395 400  
 Ser Cys Gln Phe Gly Pro Asp Val Thr Lys Ala Phe Leu Glu Glu Asn  
 405 410 415  
 Gln Leu Asp Tyr Ile Ile Arg Ser His Glu Val Lys Ala Glu Gly Tyr  
 420 425 430  
 Glu Val Ala His Gly Gly Arg Cys Val Thr Val Phe Ser Ala Pro Asn  
 435 440 445  
 Tyr Cys Asp Gln Met Gly Asn Lys Ala Ser Tyr Ile His Leu Gln Gly  
 450 455 460  
 Ser Asp Leu Arg Pro Gln Phe His Gln Phe Thr Ala Val Pro His Pro  
 465 470 475 480  
 Asn Val Lys Pro Met Ala Tyr Ala Asn Ile Leu Leu Gln Leu Gly Met  
 485 490 495

Met

<210> 20  
 <211> 513  
 <212> PRT  
 <213> Saccharomyces cerevisiae

<220>  
 <221> PEPTIDE  
 <222> (1)  
 <223> PP5

<400> 20  
 Met Ser Thr Pro Thr Ala Ala Asp Arg Ala Lys Ala Leu Glu Arg Lys  
 1 5 10 15  
 Asn Glu Gly Asn Val Phe Val Lys Glu Lys His Phe Leu Lys Ala Ile  
 20 25 30  
 Glu Lys Tyr Thr Glu Ala Ile Asp Leu Asp Ser Thr Gln Ser Ile Tyr  
 35 40 45  
 Phe Ser Asn Arg Ala Phe Ala His Phe Lys Val Asp Asn Phe Gln Ser  
 50 55 60

## 0070777-000026SEQLIST.txt

Ala Leu Asn Asp Cys Asp Glu Ala Ile Lys Leu Asp Pro Lys Asn Ile  
 65 70 75 80  
 Lys Ala Tyr His Arg Arg Ala Leu Ser Cys Met Ala Leu Leu Glu Glu  
 85 90 95  
 Lys Lys Ala Arg Lys Asp Leu Asn Val Leu Leu Lys Ala Lys Pro Asn  
 100 105 110  
 Asp Pro Ala Ala Thr Lys Ala Leu Leu Thr Cys Asp Arg Phe Ile Arg  
 115 120 125  
 Glu Glu Arg Phe Arg Lys Ala Ile Gly Gly Ala Glu Asn Glu Ala Lys  
 130 135 140  
 Ile Ser Leu Cys Gln Thr Leu Asn Leu Ser Ser Phe Asp Ala Asn Ala  
 145 150 155 160  
 Asp Leu Ala Asn Tyr Glu Gly Pro Lys Leu Glu Phe Glu Gln Leu Tyr  
 165 170 175  
 Asp Asp Lys Asn Ala Phe Lys Gly Ala Lys Ile Lys Asn Met Ser Gln  
 180 185 190  
 Glu Phe Ile Ser Lys Met Val Asn Asp Leu Phe Leu Lys Gly Lys Tyr  
 195 200 205  
 Leu Pro Lys Lys Tyr Val Ala Ala Ile Thr Ser His Ala Asp Thr Leu  
 210 215 220  
 Phe Arg Gln Glu Pro Ser Met Val Glu Leu Glu Asn Asn Ser Thr Pro  
 225 230 235 240  
 Asp Val Lys Ile Ser Val Cys Gly Asp Thr His Gly Gln Phe Tyr Asp  
 245 250 255  
 Val Leu Asn Leu Phe Arg Lys Phe Gly Lys Val Gly Pro Lys His Thr  
 260 265 270  
 Tyr Leu Phe Asn Gly Asp Phe Val Asp Arg Gly Ser Trp Ser Cys Glu  
 275 280 285  
 Val Ala Leu Leu Phe Tyr Cys Leu Lys Ile Leu His Pro Asn Asn Phe  
 290 295 300  
 Phe Leu Asn Arg Gly Asn His Glu Ser Asp Asn Met Asn Lys Ile Tyr  
 305 310 315 320  
 Gly Phe Glu Asp Glu Cys Lys Tyr Lys Tyr Ser Gln Arg Thr Phe Asn  
 325 330 335  
 Met Phe Ala Gln Ser Phe Glu Ser Leu Pro Leu Ala Thr Leu Ile Asn  
 340 345 350  
 Asn Asp Tyr Leu Val Met His Gly Gly Leu Pro Ser Asp Pro Ser Ala  
 355 360 365  
 Thr Leu Ser Asp Phe Lys Asn Ile Asp Arg Phe Ala Gln Pro Pro Arg  
 370 375 380  
 Asp Gly Ala Phe Met Glu Leu Leu Trp Ala Asp Pro Gln Glu Ala Asn  
 385 390 395 400  
 Gly Met Gly Pro Ser Gln Arg Gly Leu Gly His Ala Phe Gly Pro Asp  
 405 410 415  
 Ile Thr Asp Arg Phe Leu Arg Asn Asn Lys Leu Arg Lys Ile Phe Arg  
 420 425 430

0070777-000026SEQLIST.txt

Ser His Glu Leu Arg Met Gly Gly Val Gln Phe Glu Gln Lys Gly Lys  
435 440 445  
Leu Met Thr Val Phe Ser Ala Pro Asn Tyr Cys Asp Ser Gln Gly Asn  
450 455 460  
Leu Gly Gly Val Ile His Val Val Pro Gly His Gly Ile Leu Gln Ala  
465 470 475 480  
Gly Arg Asn Asp Asp Gln Asn Leu Ile Ile Glu Thr Phe Glu Ala Val  
485 490 495  
Glu His Pro Asp Ile Lys Pro Met Ala Tyr Ser Asn Gly Gly Phe Gly  
500 505 510  
Leu

<210> 21  
<211> 520  
<212> PRT  
<213> Drosophila melanogaster

<220>  
<221> PEPTIDE  
<222> (1)  
<223> PP5

<400> 21  
Met Ser Ser Ser Glu Leu Glu Val Gln Lys Ala Ala Asp Cys Gln Gln  
1 5 10 15  
Glu Ala Lys Val Pro Ala Ser Val Glu Ile Thr Gly Ser Lys Gln Pro  
20 25 30  
Glu Glu Asp Thr Asn Ala Arg Thr Lys Ala Glu Leu Asp Phe Ala Ala  
35 40 45  
Ala Glu Gln Tyr Lys Asn Gln Gly Asn Glu Met Leu Lys Thr Lys Glu  
50 55 60  
Phe Ser Lys Ala Ile Asp Met Tyr Thr Lys Ala Leu Glu Leu His Pro  
65 70 75 80  
Asn Ser Ala Ile Tyr Tyr Ala Asn Arg Ser Leu Ala His Leu Arg Gln  
85 90 95  
Glu Ser Phe Gly Phe Ala Leu Gln Asp Gly Val Ser Ala Val Lys Ala  
100 105 110  
Asp Pro Ala Tyr Leu Lys Gly Tyr Tyr Arg Arg Ala Ala Ala His Met  
115 120 125  
Ser Leu Gly Lys Phe Lys Gln Ala Leu Cys Asp Phe Glu Phe Val Ala  
130 135 140  
Lys Cys Arg Pro Asn Asp Lys Asp Ala Lys Ile Lys Phe Thr Glu Cys  
145 150 155 160  
Asn Lys Thr Val Lys Met Arg Ala Phe Glu Arg Ala Ile Ala Val Asp  
165 170 175  
Lys Pro Glu Lys Thr Leu Ser Glu Met Tyr Ser Asp Met Glu Asn Ile  
180 185 190

## 0070777-000026SEQLIST.txt

Thr Ile Glu Asp Asp Tyr Lys Gly Pro Gln Leu Glu Asp Gly Lys Val  
 195 200 205  
 Thr Leu Lys Phe Met Lys Glu Leu Met Glu His Thr Lys Ala Gln Lys  
 210 215 220  
 Arg Leu His Arg Lys Phe Ala Tyr Lys Ile Leu Cys Glu Ile Asp Thr  
 225 230 235 240  
 Tyr Met Arg Ala Gln Pro Ser Leu Val Asp Ile Thr Val Pro Asp Glu  
 245 250 255  
 Glu Lys Glu Thr Ile Cys Gly Asp Ile His Gly Gln Phe Tyr Asp Leu  
 260 265 270  
 Met Asn Ile Phe Glu Ile Asn Gly Leu Pro Ser Glu Lys Asn Pro Tyr  
 275 280 285  
 Leu Phe Asn Gly Asp Phe Val Asp Arg Gly Ser Phe Ser Val Glu Cys  
 290 295 300  
 Ile Glu Thr Leu Phe Gly Phe Lys Leu Leu Tyr Pro Asn His Phe Phe  
 305 310 315 320  
 Leu Ala Arg Gly Asn His Glu Ser Ile Asn Met Asn Gln Met Tyr Gly  
 325 330 335  
 Glu Thr Gly Glu Val Thr Ala Lys Tyr Thr Ser Ala Met Ala Asp Ile  
 340 345 350  
 Phe Thr Gln Val Glu Asn Trp Leu Pro Leu Cys His Cys Ile Asn Gln  
 355 360 365  
 Lys Ile Leu Val Met His Gly Gly Leu Phe Ser Thr Glu Asp Val Thr  
 370 375 380  
 Leu Asp His Ile Arg Arg Ile Glu Arg Asn Cys Gln Pro Pro Glu Glu  
 385 390 395 400  
 Gly Leu Met Cys Glu Leu Leu Trp Ser Asp Pro Gln Gln Trp Met Gly  
 405 410 415  
 Leu Gly Gln Ser Lys Arg Gly Val Gly Ile Gln Phe Gly Pro Asp Val  
 420 425 430  
 Thr Glu Lys Glu Cys Lys Asp Asn Asn Leu Asp Tyr Ile Ile Arg Ser  
 435 440 445  
 His Glu Val Lys Asp Met Gly Tyr Glu Val Ala His Asn Gly Lys Cys  
 450 455 460  
 Ile Thr Val Phe Ser Ala Pro Asn Tyr Cys Asp Thr Met Gly Asn Met  
 465 470 475 480  
 Gly Ala Phe Ile Thr Ile Thr Gly Asn Asn Leu Lys Pro Asn Tyr Lys  
 485 490 495  
 Ser Phe Glu Ala Val Pro His Pro Asp Val Lys Pro Met Ala Tyr Ala  
 500 505 510  
 Asn Ser Leu Met Asn Trp Leu Ala  
 515 520

<210> 22  
 <211> 524  
 <212> PRT  
 <213> Caenorhabditis elegans



<220>  
 <221> PEPTIDE  
 <222> (1)  
 <223> PP5

<400> 22  
 Met Ala Ala Thr Ile Thr Asp Asp Ile Val Ala Thr Val Leu Glu Ser  
 1 5 10 15  
 Ile Glu Glu Lys Ser Tyr Glu Asp Glu Lys Glu Lys Ala Gly Met Ile  
 20 25 30  
 Lys Asp Glu Ala Asn Gln Phe Phe Lys Asp Gln Val Tyr Asp Val Ala  
 35 40 45  
 Ala Asp Leu Tyr Ser Val Ala Ile Glu Ile His Pro Thr Ala Val Leu  
 50 55 60  
 Tyr Gly Asn Arg Ala Gln Ala Tyr Leu Lys Lys Glu Leu Tyr Gly Ser  
 65 70 75 80  
 Ala Leu Asp Asp Ala Asp Asn Ala Ile Ala Ile Asp Pro Ser Tyr Val  
 85 90 95  
 Lys Gly Phe Tyr Arg Arg Ala Thr Ala Asn Met Ala Leu Gly Arg Phe  
 100 105 110  
 Lys Lys Ala Leu Thr Asp Tyr Gln Ala Val Val Lys Val Cys Pro Asn  
 115 120 125  
 Asp Lys Asp Ala Arg Ala Lys Phe Asp Glu Cys Ser Lys Ile Val Arg  
 130 135 140  
 Arg Gln Lys Phe Glu Ala Ala Ile Ser Thr Asp His Asp Lys Lys Thr  
 145 150 155 160  
 Val Ala Glu Thr Leu Asp Ile Asn Met Ala Ile Glu Asp Ser Tyr Asp  
 165 170 175  
 Gly Pro Arg Leu Glu Asp Lys Ile Thr Lys Glu Phe Val Leu Gln Leu  
 180 185 190  
 Ile Lys Thr Phe Lys Asn Gln Gln Lys Leu His Lys Lys Tyr Ala Phe  
 195 200 205  
 Lys Met Leu Leu Glu Phe Tyr Asn Tyr Val Lys Ser Leu Pro Thr Met  
 210 215 220  
 Val Glu Ile Thr Val Pro Thr Gly Lys Lys Phe Thr Ile Cys Gly Asp  
 225 230 235 240  
 Val His Gly Gln Phe Tyr Asp Leu Cys Asn Ile Phe Glu Ile Asn Gly  
 245 250 255  
 Tyr Pro Ser Glu Thr Asn Pro Tyr Leu Phe Asn Gly Asp Phe Val Asp  
 260 265 270  
 Arg Gly Ser Phe Ser Val Glu Thr Ile Phe Thr Met Ile Gly Phe Lys  
 275 280 285  
 Leu Leu Pro Asn His Phe Phe Met Ser Arg Gly Asn His Glu Ser Asp  
 290 295 300  
 Val Met Asn Lys Met Tyr Gly Phe Glu Gly Glu Val Lys Ala Lys Tyr  
 305 310 315 320

## 0070777-000026SEQLIST.txt

Thr Gln Gln Met Cys Asp Met Phe Thr Glu Thr Phe Cys Trp Leu Pro  
 325 330 335  
 Leu Cys His Leu Ile Asn Glu Lys Ile Phe Val Cys His Gly Gly Leu  
 340 345 350  
 Phe Lys Glu Asp Gly Val Thr Leu Glu Asp Ile Arg Lys Thr Asp Arg  
 355 360 365  
 Asn Arg Gln Pro Pro Asp Glu Gly Ile Met Cys Asp Leu Leu Trp Glu  
 370 375 380  
 Lys Asn Trp Lys Asn Leu Lys Ile Leu Tyr Pro Asp Gly Lys Ile Asn  
 385 390 395 400  
 Lys Asn Ser Asn Cys Gln Pro Lys Thr Cys Lys Asn Ala Ser Asp Pro  
 405 410 415  
 Gln Pro Ile Asn Gly Arg Ser Pro Ser Lys Arg Gly Val Gly Cys Gln  
 420 425 430  
 Phe Gly Pro Asp Val Thr Ser Lys Trp Cys Glu Thr Asn Gly Ile Glu  
 435 440 445  
 Tyr Val Val Arg Ser His Glu Val Lys Pro Glu Gly Tyr Glu Met His  
 450 455 460  
 His Asn Gly Gln Cys Phe Thr Val Phe Ser Ala Pro Asn Tyr Cys Asp  
 465 470 475 480  
 Gln Met Asn Asn Lys Gly Ala Phe Ile Thr Ile Thr Gly Asp Asn Leu  
 485 490 495  
 Thr Pro Arg Phe Thr Pro Phe Asp Ala Val Pro His Pro Lys Leu Pro  
 500 505 510  
 Pro Met Ala Tyr Ala Asn Ser Leu Phe Gly Phe Asn  
 515 520

<210> 23  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> PP2A motif

<400> 23  
 Gly Asp Xaa His Gln Gly Gln  
 1 5

<210> 24  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> PP2A motif

<400> 24  
 Gly Asp Xaa Val Xaa Arg Gly  
 1 5

<210> 25  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> PP2A motif

<400> 25  
 Arg Gly Asn His Glu  
 1 5

<210> 26  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> C-terminal consensus sequence

<400> 26  
 Ser Ala Pro Asn Tyr Cys  
 1 5